

Claims

1. A process for detecting numerical changes in cell DNA, comprising the following steps:

- (a) isolation of the DNA from normal cells and amplification of the DNA by means of a PCR method using tag primers,
- (b) *in situ* hybridization of cells under study with the amplified DNA from (a),
- (c) amplification of DNA from the *in situ* hybridized cells from (b) by means of a PCR method using the tag primers from (a), and
- (d) identification of numerical changes in the amplified DNA from (c) in a normal way.

2. The process according to claim 1, characterized in that the cells under study originate from tumors.

3. The process according to claim 1, characterized in that the cells under study originate from the blood of pregnant persons.

4. The process according to claim 2 or 3, characterized in that the cells under study are those of a small cell population or single cells.

5. The process according to any one of claims 1 to 4, characterized in that the cells under study have an interphase nucleus.

6. The process according to any one of claims 1 to 5, characterized in that the tag primers are degenerative primers.

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7. The process according to any one of claims 1 to 6, characterized in that the identification from (d) comprises a CGH method.
8. A kit for carrying out the process according to any one of claims 1 to 7, comprising the following components:
 - (a) amplified DNA from normal cells, the DNA being flanked by tag primers,
 - (b) tag primers, and common
 - (c) auxiliary agents, particularly those suitable for identifying numerical changes in a DNA.

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Abstract of the Disclosure**Identification of Numerical Changes in Cell DNA**

The present invention relates to a process for identifying numerical changes in cell DNA, comprising the following steps:

- (a) isolation of DNA from normal cells and amplification of the DNA by means of a PCR method using tag primers,
- (b) *in situ* hybridization of cells under study with the amplified DNA from (a),
- (c) amplification of DNA from the *in situ* hybridized cells from (b) by means of a PCR method using the tag primers from (a), and
- (c) identification of numerical changes in the amplified DNA from (c) in a normal way.

In addition, the invention concerns a kit suitable for carrying out the process.

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Amended Claims

1. A process for detecting numerical changes in cell DNA, comprising the following steps:

- (a) isolation of the DNA from cells which have no known numerical changes in their DNA, and amplification of the DNA by means of a PCR method using tag primers,
- (b) *in situ* hybridization of cells under study with the amplified DNA from (a),
- (c) amplification of DNA from the *in situ* hybridized cells from (b) by means of a PCR method using the tag primers from (a), and
- (d) identification of numerical changes in the amplified DNA from (c).

2. The process according to claim 1, characterized in that the cells under study originate from tumors.

3. The process according to claim 1, characterized in that the cells under study originate from the blood of pregnant persons.

4. The process according to claim 2 or 3, characterized in that the cells under study are those of a small cell population or single cells.

5. The process according to any one of claims 1 to 4, characterized in that the cells under study have an interphase nucleus.

6. The process according to any one of claims 1 to 5, characterized in that the tag primers are degenerative primers.

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7. The process according to any one of claims 1 to 6, characterized in that the identification from (d) comprises a "Comparative Genomic Hybridization" (CGH) method.
8. A kit for carrying out the process according to any one of claims 1 to 7, comprising the following components:
 - (a) amplified DNA from cells which have no known numerical changes in their DNA, the DNA being flanked by tag primers,
 - (b) tag primers, and
 - (c) auxiliary agents for identifying numerical changes in a DNA.

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